SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Kaufman, Randal J.
                  Wasley, Louise

    (ii) TITLE OF INVENTION: Method of Increasing Yield of
                           Mature Proteins

    (iii) NUMBER OF SEQUENCES: 2

    (iv) CORRESPONDENCE ADDRESS:

        (A) ADDRESSEE: Genetics Institute, Inc.
        (B) STREET: 87 CambridgePark Drive
        (C) CITY: Cambridge
        (D) STATE: Massachusetts
        (E) COUNTRY: United States of America
        (F) ZIP: 02140

    (v) COMPUTER READABLE FORM:

        (A) MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb storage

        (B) COMPUTER: IBM PS/2

        (C) OPERATING SYSTEM: PC-DOS

        (D) SOFTWARE: WordPerfect 5.1

    (vi) CURRENT APPLICATION DATA:

        (A) APPLICATION NUMBER:

        (B) FILING DATE:

        (C) CLASSIFICATION:

    (vii) PRIOR APPLICATION DATA: not applicable

        (A) APPLICATION NUMBER:

        (B) FILING DATE:

    (viii) ATTORNEY/AGENT INFORMATION:

        (A) NAME: Ellen J. Kapinos, Esquire
        (B) REGISTRATION NUMBER: 32,245
        (C) REFERENCE/DOCKET NUMBER: GI 5181

    (ix) TELECOMMUNICATION INFORMATION:

```
        (A)   TELEPHONE:  (617) 876-1170
        (B)   TELEFAX:  (617) 876-5851

(2)   INFORMATION FOR SEQ ID NO:1

      (i)   SEQUENCE CHARACTERISTICS:

            (A)   LENGTH:  2385 base pairs

            (B)   TYPE:   nucleic acid

            (C)   STRANDEDNESS:   double

            (D)   TOPOLOGY:   unknown

      (ii)   MOLECULE TYPE: partial human genomic DNA

             (A) DESCRIPTION: sequence encoding furin

      (iii)  HYPOTHETICAL:   no

      (iv)   ANTI-SENSE:   no

      (v)    PUBLICATION INFORMATION:

             (A)  AUTHORS: van den Ouweland, A. M. W.
             (B)  JOURNAL: Nucl. Acids. Res.
             (C)  VOLUME: 18
             (D)  PAGES:   664
             (E)  DATE:   1990

      (vi)   SEQUENCE DESCRIPTION:   SEQ ID NO:1
```

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ATG GAG CTC AGG CCC TGG TTC                                      21
Met Glu Leu Arg Pro Trp Leu
 1               5


CTA TGG GTC GTA CCA CCA ACA GGA ACC TTG GTC CTG CTA              60
Leu Trp Val Val Ala Ala Thr Gly Thr Leu Val Leu Leu
         10                  15                  20


GCA GCT GAT GCT CAG GGC CAG AAG GTC TTC ACC AAC ACG              99
Ala Ala Asp Ala Gln Gly Gln Lys Val Phe Thr Asn Thr
                 25                  30


TGG GCT GTG CGC ATC CCT GGA GGC CCA GCG GTG GCC AAC             138
Trp Ala Val Arg Ile Pro Gly Gly Pro Ala Val Ala Asn
     35                  40                  45


AGT GTG GCA CGG AAG CAT GGG TTC CTC AAC CTG GGC CAG             177
Ser Val Ala Arg Lys His Gly Phe Leu Asn Leu Gly Gln
                 50                  55
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ATC TTC GGG GAC TAT TAC CAC TTC TGG CAT CGA GGA GTG        216
Ile Phe Gly Asp Tyr Tyr His Phe Trp His Arg Gly Val
60              65                  70

ACG AAG CGG TCC CTG TCG CCT CAC CGC CCG CGG CAC AGC        255
Thr Lys Arg Ser Leu Ser Pro His Arg Pro Arg His Ser
        75              80                      85

CGG CTG CAG AGG GAG CCT CAA GTA CAG TGG CTG GAA CAG        294
Arg Leu Gln Arg Glu Pro Gln Val Gln Trp Leu Glu Gln
                90                  95

CAG GTG GCA AAG CGA CGG ACT AAA CGG GAC GTG TAC CAG        333
Gln Val Ala Lys Arg Arg Thr Lys Arg Asp Val Tyr Gln
    100             105                 110

GAG CCC ACA GAC CCC AAG TTT CCT CAG CAG TGG TAC CTG        372
Glu Pro Thr Asp Pro Lys Phe Pro Gln Gln Trp Tyr Leu
            115                 120

TCT GGT GTC ACT CAG CGG GAC CTG AAT GTG AAG GCG GCC        411
Ser Gly Val Thr Gln Arg Asp Leu Asn Val Lys Ala Ala
125             130                 135

TGG GCG CAG GGC TAC ACA GGG CAC GGC ATT CTG GTC TCC        450
Trp Ala Gln Gly Tyr Thr Gly His Gly Ile Val Val Ser
        140                 145                 150

ATT CTG GAC GAT GGC ATC GAG AAG AAC CAC CCC GAC TTG        489
Ile Leu Asp Asp Gly Ile Glu Lys Asn His Pro Asp Leu
            155                 160

GCA GGC AAT TAT GAT CCT GGG GCC AGT TTT CAT GTC AAT        528
Ala Gly Asn Tyr Asp Pro Gly Ala Ser Phe Asp Val Asn
    165             170                 175

GAC CAG GAC CCT GAC CCC CAG CCT CGG TAC ACA CAG ATG        567
Asp Gln Asp Pro Asp Pro Gln Pro Arg Tyr Thr Gln Met
            180             185

AAT GAC AAC AGG CAC GGC ACA CGG TGT GCG GGG GAA GTG        606
Asn Asp Asn Arg His Gly Thr Arg Cys Ala Gly Glu Val
190             195                 200

GCT GCC GTG GCC AAC AAC CGT GTC TGT GGT GTA GGT GTG        645
Ala Ala Val Ala Asn Asn Gly Val Cys Gly Val Gly Val
        205             210                     215

GCC TAC AAC GCC CGC ATT GGA GGG GTC CGC ATG CTG GAT        684
Ala Tyr Asn Ala Arg Ile Gly Gly Val Arg Met Leu Asp
            220                 225
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```
GGC GAG GTG ACA GAT GCA GTG GAG GCA CGC TCG CTG GGC       723
Gly Glu Val Thr Asp Ala Val Glu Ala Arg Ser Leu Gly
    230             235                 240

CTG AAC CCC AAC CAC ATC CAC ATC TAC AGT GCC AGC TGG       762
Leu Asn Pro Asn His Ile His Ile Tyr Ser Ala Ser Trp
            245                 250

GGC CCC GAG GAT GAC GGC AAG ACA GTG GAT GGG CCA GCC       801
Gly Pro Glu Asp Asp Gly Lys Thr Val Asp Gly Pro Ala
255             260                 265

CGG CTC GCC GAG GAG GCC TTC TTC CGT GGG CTT AGC CAG       840
Arg Leu Ala Glu Glu Ala Phe Phe Arg Gly Val Ser Gln
        270                 275                 280

GGC CGA GGG GGG CTG GGC TCC ATC TTT GTC TGG GCC TCG       879
Gly Arg Gly Gly Leu Gly Ser Ile Phe Val Trp Ala Ser
            285                 290

GGG AAC GGG GGG CGG GAA CAT GAC AGC TGC AAC TGC GAC       918
Gly Asn Gly Gly Arg Glu His Asp Ser Cys Asn Cys Asp
    295                 300                 305

GGC TAC ACC AAC AGT ATC TAC ACG CTG TCC ATC AGC AGC       957
Gly Tyr Thr Asn Ser Ile Tyr Thr Leu Ser Ile Ser Ser
            310                 315

GCC ACG CAG TTT GGC AAC GTG CCG TGG TAC AGC GAG GCC    ·  996
Ala Thr Gln Phe Gly Asn Val Pro Trp Tyr Ser Glu Ala
320             325                 330

TGC TCG TCC ACA CTG GCC ACG ACC TAC AGC AGT GGC AAC      1035
Cys Ser Ser Thr Leu Ala Thr Thr Tyr Ser Ser Gly Asn
        335                 340                 345

CAG AAT GAG AAG CAG ATC GTG ACG ACT GAC TTG CGG CAG      1074
Gln Asn Glu Lys Gln Ile Val Thr Thr Asp Leu Arg Gln
            350                 355

AAG TGC ACG GAG TCT CAC ACG GGC ACC TCA GCC TCT GCC      1113
Lys Cys Thr Glu Ser His Thr Gly Thr Ser Ala Ser Ala
    360                 365                 370

CCC TTA GCA GCC GGC ATC ATT GCT CTC ACC CTG GAG GCC      1152
Pro Leu Ala Ala Gly Ile Ile Ala Leu Thr Leu Glu Ala
            375                 380

AAT AAG AAC CTC ACA TGG CGG GAC ATG CAA CAC CTG GTG      1191
Asn Lys Asn Leu Thr Trp Arg Asp Met Gln His Leu Val
385                 390                 395

GTA CAG ACC TCG AAG CCA GCC CAC CTC AAT GCC AAC GAC      1230
Val Gln Thr Ser Lys Pro Ala His Leu Asn Ala Asn Asp
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                  400                       405                       410

TGG GCC ACC AAT GGT GTG GGG CGG AAA GTG AGC CAC TCA     1269
Trp Ala Thr Asn Gly Val Gly Arg Lys Val Ser His Ser
                415                 420

TAT GGC TAC GGG CTT TTC GAC GCA GGC GCC ATG GTG GCC     1308
Tyr Gly Tyr Gly Leu Leu Asp Ala Gly Ala Met Val Ala
        425                 430                 435

CTG GCC CAG AAT TGG ACC ACA GTC GCC CCC CAG CGG AAG     1347
Leu Ala Gln Asn Trp Thr Thr Val Ala Pro Gln Arg Lys
                440                 445

TGC ATC ATC GAC ATC CTC ACC GAG CCC AAA GAC ATC GGG     1386
Cys Ile Ile Asp Ile Leu Thr Glu Pro Lys Asp Ile Gly
450                 455                 460

AAA CGG CTC GAC CTC CGG AAC ACC GTG ACC GCG TCC CTG     1425
Lys Arg Leu Glu Val Arg Lys Thr Val Thr Ala Cys Leu
        465                 470                 475

GGC GAG CCC AAC CAC ATC ACT CGG CTG GAG CAC GCT CAG     1464
Gly Glu Pro Asn His Ile Thr Arg Leu Glu His Ala Gln
                480                 485

GCG CGG CTC ACC CTG TCC TAT AAT CGC CGT GGC GAC CTG     1503
Ala Arg Leu Thr Leu Ser Tyr Asn Arg Arg Gly Asp Leu
        490                 495                 500

GCC ATC CAC CTG GTC AGC CCC ATG GGC ACC CGC TCC ACC     1542
Ala Ile His Leu Val Ser Pro Met Gly Thr Arg Ser Thr
                505                 510

CTG CTG GCA GCC AGG CCA CAT GAC TAC TCC GCA GAT GGG     1581
Leu Leu Ala Ala Arg Pro His Asp Tyr Ser Ala Asp Gly
515                 520                 525

TTT AAT GAC TGG GCC TTC ATG ACA ACT CAT TCC TGG GAT     1620
Phe Asn Asp Trp Ala Phe Met Thr Thr His Ser Trp Asp
                530                 535                 540

GAC GAT CCC TCT GGG GAG TGG GTC CTA GAG ATT GAA AAC     1659
Glu Asp Pro Ser Gly Glu Trp Val Leu Glu Ile Glu Asn
                545                 550

ACC AGC GAA GCC AAC AAC TAT GGG ACG CTG ACC AAC TCC     1698
Thr Ser Glu Ala Asn Asn Tyr Gly Thr Leu Thr Lys Phe
        555                 560                 565

ACC CTC GTA CTC TAT GGC ACC GCC CCT GAC GGG CTC CCC     1737
Thr Leu Val Leu Tyr Gly Thr Ala Pro Glu Gly Leu Pro
                570                 575
```

```
GTA CCT CCA GAA AGC AGT GGC TGC AAG ACC CTC ACG TCC   1776
Val Pro Pro Glu Ser Ser Gly Cys Lys Thr Leu Thr Ser
580                 585                 590

AGT CAG GCC TGT GTG GTG TGC GAG GAA GGC TTC TCC CTC   1815
Ser Gln Ala Cys Val Val Cys Glu Glu Gly Phe Ser Leu
            595                 600                 605

CAC CAG AAG AGC TGT GTC CAG CAC TGC CCT CCA GGC TTC   1854
His Gln Lys Ser Cys Val Gln Asn Cys Pro Pro Gly Phe
                610                 615

GCC CCC CAA GTC CTC GAT ACG CAC TAT AGC ACC GAG AAT   1893
Ala Pro Gln Val Leu Asp Thr Asn Tyr Ser Thr Glu Asn
    620                 625                 630

GAC GTG GAG ACC ATC CGG GCC AGC GTC TGC GCC CCC TGC   1932
Asp Val Glu Thr Ile Arg Ala Ser Val Cys Ala Pro Cys
            635                 640

CAC GCC TCA TGT GCC ACA TGC CAG GGG CCG GCC CTG ACA   1971
His Ala Ser Cys Ala Thr Cys Gln Gly Pro Ala Leu Thr
645                 650                 655

GAC TGC CTC AGC TGC CCC AGC CAC GCC TCC TTG GAC CCT   2010
Asp Cys Leu Ser Cys Pro Ser His Ala Ser Leu Asp Pro
        660                 665                 670

GTG GAG CAG ACT TGC TCC CGG CAA AGC CAG AGC AGC CGA   2049
Val Glu Gln Thr Cys Ser Arg Gln Ser Gln Ser Ser Arg
                675                 680

GAG TCC CCG CCA CAG CAG CAG CCA CCT CGG CTG CCC CCG   2088
Glu Ser Pro Pro Gln Gln Gln Pro Pro Arg Leu Pro Pro
        685                 690                 695

GAG GTG GAG GCG GGG CAA CGG CTG CGG GCA GGG CTG CTG   2127
Glu Val Glu Ala Gly Gln Arg Leu Arg Ala Gly Leu Leu
            700                 705

CCC TCA CAC CTG CCT GAG GTG GTG GCC GGC CTC AGC TGC   2166
Pro Ser His Leu Pro Glu Val Val Ala Gly Leu Ser Cys
710                 715                 720

GCC TTC ATC GTG CTG GTC TTC GTC ACT GTC TTC CTG CTC   2205
Ala Phe Ile Val Leu Val Phe Val Thr Val Phe Leu Val
        725                 730                 735

CTG CAG CTG CGC TCT GGC TTT AGT TTT CGG GGG GTG AAG   2244
Leu Gln Leu Arg Ser Gly Phe Ser Phe Arg Gly Val Lys
            740                 745

GTG TAC ACC ATG GAC CGT GGC CTC ATC TCC TAC AAG GGG   2283
Val Tyr Thr Met Asp Arg Gly Leu Ile Ser Tyr Lys Gly
```

```
CTG CCC CCT GAA GCC TGG CAG GAG GAG TGC CCG TCT GAC   2322
Leu Pro Pro Glu Ala Trp Gln Glu Glu Cys Pro Ser Asp
            765                         770

TCA GAA GAG GAC GAG GGC CGG GGC GAG AGG ACC GCC TTT   2361
Ser Glu Glu Asp Glu Gly Arg Gly Glu Arg Thr Ala Phe
775                         780                         785

ATC AAA GAC CAG AGC GCC CTC TGA                        2385
Ile Lys Asp Gln Ser Ala Leu End
            790
```

(3)   INFORMATION FOR SEQ ID NO:2

        (i)   SEQUENCE CHARACTERISTICS:

                (A)   LENGTH: 794 amino acids

                (B)   TYPE: amino acids

                (C)   STRANDEDNESS: single

                (D)   TOPOLOGY: unknown

        (ii)   MOLECULE TYPE: furin

        (iii) HYPOTHETICAL: no

        (iv)   ANTI-SENSE: no

        (v)   PUBLICATION INFORMATION:

                (A) AUTHORS: van den Ouweland, A. M. W.
                (B) JOURNAL: Nucl. Acids. Res.
                (C) VOLUME: 18
                (D) PAGES: 664
                (E) DATE: 1990

        (vi)   SEQUENCE DESCRIPTION: SEQ ID NO:2

```
Met Glu Leu Arg Pro Trp Leu
  1                 5

Leu Trp Val Val Ala Ala Thr Gly Thr Leu Val Leu Leu
        10                      15                  20

Ala Ala Asp Ala Gln Gly Gln Lys Val Phe Thr Asn Thr
                25                      30

Trp Ala Val Arg Ile Pro Gly Gly Pro Ala Val Ala Asn
```

```
            35                      40                      45
Ser Val Ala Arg Lys His Gly Phe Leu Asn Leu Gly Gln
                50                  55

Ile Phe Gly Asp Tyr Tyr His Phe Trp His Arg Gly Val
60              65                  70

Thr Lys Arg Ser Leu Ser Pro His Arg Pro Arg His Ser
        75                  80                      85


Arg Leu Gln Arg Glu Pro Gln Val Gln Trp Leu Glu Gln
                90                  95

Gln Val Ala Lys Arg Arg Thr Lys Arg Asp Val Tyr Gln
    100             105                 110

Glu Pro Thr Asp Pro Lys Phe Pro Gln Gln Trp Tyr Leu
            115                 120

Ser Gly Val Thr Gln Arg Asp Leu Asn Val Lys Ala Ala
125                 130                 135

Trp Ala Gln Gly Tyr Thr Gly His Gly Ile Val Val Ser
        140                 145                 150

Ile Leu Asp Asp Gly Ile Glu Lys Asn His Pro Asp Leu
            155                 160

Ala Gly Asn Tyr Asp Pro Gly Ala Ser Phe Asp Val Asn
    165             170                 175

Asp Gln Asp Pro Asp Pro Gln Pro Arg Tyr Thr Gln Met
            180                 185

Asn Asp Asn Arg His Gly Thr Arg Cys Ala Gly Glu Val
190             195                 200

Ala Ala Val Ala Asn Asn Gly Val Cys Gly Val Gly Val
        205                 210                 215

Ala Tyr Asn Ala Arg Ile Gly Gly Val Arg Met Leu Asp
            220                 225

Gly Glu Val Thr Asp Ala Val Glu Ala Arg Ser Leu Gly
    230             235                 240

Leu Asn Pro Asn His Ile His Ile Tyr Ser Ala Ser Trp
            245                 250

Gly Pro Glu Asp Asp Gly Lys Thr Val Asp Gly Pro Ala
255                 260                 265
```

```
Arg Leu Ala Glu Glu Ala Phe Phe Arg Gly Val Ser Gln
         270             275             280

Gly Arg Gly Gly Leu Gly Ser Ile Phe Val Trp Ala Ser
             285             290

Gly Asn Gly Gly Arg Glu His Asp Ser Cys Asn Cys Asp
    295             300             305

Gly Tyr Thr Asn Ser Ile Tyr Thr Leu Ser Ile Ser Ser
             310             315

Ala Thr Gln Phe Gly Asn Val Pro Trp Tyr Ser Glu Ala
320             325             330

Cys Ser Ser Thr Leu Ala Thr Thr Tyr Ser Ser Gly Asn
        335             340             345

Gln Asn Glu Lys Gln Ile Val Thr Thr Asp Leu Arg Gln
            350             355

Lys Cys Thr Glu Ser His Thr Gly Thr Ser Ala Ser Ala
    360             365             370

Pro Leu Ala Ala Gly Ile Ile Ala Leu Thr Leu Glu Ala
            375             380

Asn Lys Asn Leu Thr Trp Arg Asp Met Gln His Leu Val
385             390             395

Val Gln Thr Ser Lys Pro Ala His Leu Asn Ala Asn Asp
        400             405             410

Trp Ala Thr Asn Gly Val Gly Arg Lys Val Ser His Ser
            415             420

Tyr Gly Tyr Gly Leu Leu Asp Ala Gly Ala Met Val Ala
    425             430             435

Leu Ala Gln Asn Trp Thr Thr Val Ala Pro Gln Arg Lys
            440             445

Cys Ile Ile Asp Ile Leu Thr Glu Pro Lys Asp Ile Gly
450             455             460

Lys Arg Leu Glu Val Arg Lys Thr Val Thr Ala Cys Leu
        465             470             475

Gly Glu Pro Asn His Ile Thr Arg Leu Glu His Ala Gln
            480             485

Ala Arg Leu Thr Leu Ser Tyr Asn Arg Arg Gly Asp Leu
    490             495             500
```

Ala Ile His Leu Val Ser Pro Met Gly Thr Arg Ser Thr
        505   510

Leu Leu Ala Ala Arg Pro His Asp Tyr Ser Ala Asp Gly
515   520   525

Phe Asn Asp Trp Ala Phe Met Thr Thr His Ser Trp Asp
        530   535   540

Glu Asp Pro Ser Gly Glu Trp Val Leu Glu Ile Glu Asn
            545   550

Thr Ser Glu Ala Asn Asn Tyr Gly Thr Leu Thr Lys Phe
    555   560   565

Thr Leu Val Leu Tyr Gly Thr Ala Pro Glu Gly Leu Pro
        570   575

Val Pro Pro Glu Ser Ser Gly Cys Lys Thr Leu Thr Ser
580   585   590

Ser Gln Ala Cys Val Val Cys Glu Glu Gly Phe Ser Leu
        595   600   605

His Gln Lys Ser Cys Val Gln Asn Cys Pro Pro Gly Phe
            610   615

Ala Pro Gln Val Leu Asp Thr Asn Tyr Ser Thr Glu Asn
    620   625   630

Asp Val Glu Thr Ile Arg Ala Ser Val Cys Ala Pro Cys
            635   640

His Ala Ser Cys Ala Thr Cys Gln Gly Pro Ala Leu Thr
645   650   655

Asp Cys Leu Ser Cys Pro Ser His Ala Ser Leu Asp Pro
        660   665   670

Val Glu Gln Thr Cys Ser Arg Gln Ser Gln Ser Ser Arg
            675   680

Glu Ser Pro Pro Gln Gln Gln Pro Pro Arg Leu Pro Pro
    685   690   695

Glu Val Glu Ala Gly Gln Arg Leu Arg Ala Gly Leu Leu
            700   705

Pro Ser His Leu Pro Glu Val Val Ala Gly Leu Ser Cys
710   715   720

Ala Phe Ile Val Leu Val Phe Val Thr Val Phe Leu Val
        725   730   735

```
Leu Gln Leu Arg Ser Gly Phe Ser Phe Arg Gly Val Lys
            740             745
Val Tyr Thr Met Asp Arg Gly Leu Ile Ser Tyr Lys Gly
    750             755             760
Leu Pro Pro Glu Ala Trp Gln Glu Glu Cys Pro Ser Asp
            765             770
Ser Glu Glu Asp Glu Gly Arg Gly Glu Arg Thr Ala Phe
775             780             785
Ile Lys Asp Gln Ser Ala Leu End
        790
```